IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application No.: 10/669,824)
In re application of: JIANG, Cai-Zhong)
Filed: 23 September 2003)
Art Unit: 1638)
Examiner: KRUSE, David H.)
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Mail Stop Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

DECLARATION UNDER 37 CFR 1.132 OF JEFFREY M. LIBBY

I, Jeffrey M. Libby, declare:

1. I received my Bachelor of Science degree in Microbiology from the University of Illinois and my doctoral degree in Microbiology and Microbial Genetics from Cornell University. I joined Mendel Biotechnology in June 2002 and have served as Senior Patent Agent since June 2002. I state that I have prepared Exhibit B and Exhibit C for the response to the most recent Office action of the present patent application. I have determined the theoretical melting temperatures of G3456 and the homologous polynucleotide subsequences listed in Exhibit C by first aligning each pair of full length polynucleotide sequences, finding similar subsequences of length 50 bases within each aligned pair of sequences, and comparing the reverse complement of each listed homolog subsequence with the similar subsequence of G3456 using the DINAMelt server available at www.bioinfo.rpi.edu/applications/hybrid/hybrid2.php. This declaration is being drafted as part of my normal duties to support intellectual property at Mendel Biotechnology, Inc. As compensation for employment at Mendel Biotechnology, I receive salary, benefits and stock options.

2. I hereby declare that all statements made herein are true and that they are based on my own knowledge, information and belief. These statements are made with the knowledge that willful false statements are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this application or any patent issued from it.

Date: 7 January 2008

Jeffrey M. Libby, Ph.D.
Senior Patent Agent
Mendel Biotechnology, Inc.

Exhibit B. Sequences phylogenetically-related to G3456, polypeptide SEQ ID NO: 14

The G3456 sequence used to generate the data in Table 1 of the attached declaration differs from the G3456 polypeptide sequence described in present specification by two residues, indicated below in small boxes.

>G3456 (showing residues of the polypeptide predicted to have been expressed in plants)
MKKPDLGFSMNESTVTGNHIGEEDEDRENSDEPREGAIDVATTRRPRGRPPGSRNKPKPP
IFVTRDSPNALRSHVMEIAVGADIADCVAQFARRRQRGVSILSGSGTVVNVNLRQPTAPG
AVMALHGRFDILSLTGSFLPGPSPPGATGLTIYLAGGQGQIVGGGVVGPLVAAGPVLVMA
ATFSNATYERLPLEDDDQEQHGGGGGGGSPQEKTGGPGEASSSISVYNNNVPPSLGLPNG
QHLNHEAYSSPWGHSPHARPPF*

The G3456 sequence described in the present specification is indicated below. The percentage identities of the second conserved domains of either the above or below sequence to the related sequences in Table 1 of the attached declaration remain the same regardless of which G3456 sequence is used to generate the comparisons.

>G3456 (Predicted polypeptide, 2nd conserved domain underlined)
MKKPDLGFSMNESTVTGNHIGEEDEDRENSDEPREGAIDVATTRRPRGRPPGSRNKPKPP
IFVTRDSPNALRSHVMEIAVGADIADCVAQFARRRQRGVSILSGSGTVVNVNLRQPTAPG
AVMALHGRFDILSLTGSFLPGPSPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMA
ATFSNATYERLPLEDDDQEQHGGGGGGGSPQEKNGGPGEASSSISVYNNNVPPSLGLPNG
QHLNHEAYSSPWGHSPHARPPF*

Related sequences in Table 1 of the attached declaration, their second conserved domains, and alignments to the G3456 second conserved domain are shown below.

>G3460 (Predicted polypeptide, 2nd conserved domain underlined)
MAGLDLGSASRFVQNLHLPDLHLQQNYQQPRHKRDSEEQETPPNPGTALAPFDNDDDKSQ
GLELASGPGDIVGRRPRGRPSGSKNKPKPPVIITRESANTLRAHILEVGSGSDVFDCVTA
YARRRQRGICVLSGSGTVTNVSLRQPAAAGAVVRLHGRFEILSLSGSFLPPPAPPGATSL
TIYLAGGQGQVVGGNVVGELTAAGPVIVIAASFTNVAYERLPLEEDEQQQQQLQIQSPAT
TSSQGNNNNNPFPDPSSGLPFFNLPLNMQNVQLPPF*

Identity of G3456 second conserved domain to G3460 second conserved domain determined using manual alignment = 72/96 identical residues (75.0%)

```
G3456:     VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
           V  +ARRRQRG+ +LSGSGTV NV+LRQP A GAV+ LHGRF+ILSL+GSFLP P+PPGA
G3460:     VTAYARRRQRGICVLSGSGTVTNVSLRQPAAAGAVVRLHGRFEILSLSGSFLPPPAPPGA

G3456:     TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
           T LTIYLAGGQGQ+VGG VVG L AAGPV+V+AA+F
G3460:     TSLTIYLAGGQGQVVGGNVVGELTAAGPVIVIAASF
```

>G3459 (Predicted polypeptide, 2nd conserved domain underlined)
MAGLDLGSASRFVQNLHRPDLHLQQNFQQHQDQQHQRDLEEQKTPPNHRMGAPFDDDSDD
RSPGLELTSGPGDIVGRRPRGRPPGSKNKPKPPVIITRESANTLRAHILEVGSGSDVFDC
VTAYARRRQRGICVLSGSGTVTNVSLRQPAAAGAVVTLHGRFEILSLSGSFLPPPAPPGA
TSLTIYLAGGQGQVVGGNVIGELTAAGPVIVIAASFTNVAYERLPLEEDEQQQQQQQLQI
QPPATTSSQGNNNNNNPFPDPSSGLPFFNLPLNMQNVQLPVEGWAVNPASRPQPF*

Identity of G3456 second conserved domain to G3459 second conserved domain determined using manual alignment = 71/96 identical residues (73.9%)

```
G3456:     VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
           V  +ARRRQRG+ +LSGSGTV NV+LRQP A GAV+ LHGRF+ILSL+GSFLP P+PPGA
G3459:     VTAYARRRQRGICVLSGSGTVTNVSLRQPAAAGAVVTLHGRFEILSLSGSFLPPPAPPGA

G3456:     TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
           T LTIYLAGGQGQ+VGG V+G L AAGPV+V+AA+F
G3459:     TSLTIYLAGGQGQVVGGNVIGELTAAGPVIVIAASF
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>G2153 (Predicted polypeptide, 2nd conserved domain underlined)
MANPWWTGQVNLSGLETTPPGSSQLKKPDLHISMNMAMDSGHNNHHHHQEVDNNNNDDDR
DNLSGDDHEPREGAVEAPTRRPRGRPAGSKNKPKPPIFVTRDSPNALKSHVMEIASGTDV
IETLATFARRRQRGICILSGNGTVANVTLRQPSTAAVAAAPGGAAVLALQGRFEILSLTG
SFLPGPAPPGSTGLTIYLAGGQGQVVGGSVVGPLMAAGPVMLIAATFSNATYERLPLEEE
EAAERGGGGGSGGVVPGQLGGGGSPLSSGAGGGDGNQGLPVYNMPGNLVSNGGSGGGGQM
SGQEAYGWAQARSGF*

Identity of G3456 second conserved domain to G2153 second conserved domain determined using manual alignment = 77/104 identical residues (74.0%)

```
G3456:     VAQFARRRQRGVSILSGSGTVVNVNLRQPT------APG--AVMALHGRFDILSLTGSFL
           +A FARRRQRG+ ILSG+GTV NV LRQP+      APG  AV+AL GRF+ILSLTGSFL
G2153:     LATFARRRQRGICILSGNGTVANVTLRQPSTAAVAAAPGGAAVLALQGRFEILSLTGSFL

G3456:     PGPSPPGATGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
           PGP+PPG+TGLTIYLAGGQGQ+VGG VVGPL+AAGPV+++AATF
G2153:     PGPAPPGSTGLTIYLAGGQGQVVGGSVVGPLMAAGPVMLIAATF
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>G3401 (Predicted polypeptide, 2nd conserved domain underlined)
MASKEPSGDHDHEMNGTSAGGGEPKDGAVVTGRNRRPRGRPPGSKNKPKPPIFVTRDSPN
ALRSHVMEVAGGADVAESIAHFARRRQRGVCVLSGAGTVTDVALRQPAAPSAVVALRGRF
EILSLTGTFLPGPAPPGSTGLTVYLAGGQGQVVGGSVVGTLTAAGPVMVIASTFANATYE
RLPLDQEEEEAAAGGMMAPPPLMAGAADPLLFGGGMHDAGLAAWHHARPPPPPPY*

Identity of G3456 second conserved domain to G3401 second conserved domain determined using manual alignment = 72/96 identical residues (75.0%)

```
G3456:     VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
           +A FARRRQRGV +LSG+GTV +V LRQP AP AV+AL GRF+ILSLTG+FLPGP+PPG+
G3401:     IAHFARRRQRGVCVLSGAGTVTDVALRQPAAPSAVVALRGRFEILSLTGTFLPGPAPPGS

G3456:     TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
           TGLT+YLAGGQGQ+VGG VVG L AAGPV+V+A+TF
G3401:     TGLTVYLAGGQGQVVGGSVVGTLTAAGPVMVIASTF
```

>G3457 (Predicted polypeptide, 2nd conserved domain underlined)
MDPVAAQGRPLPPPFLTRDLHLHPHHQFQPHHNHQNTEDEAGNGRGQKRDRDENAGGGGG
ATTPPQGGGEGKESGSGDGGGSDMGRRPRGRPAGSKNKPKPPIIITRDSANALRSHVMEI
ANGCDIMESITAFARRRQRGVCVLSGSGTVTNVTLRQPASPGAVVTLHGRFEILSLSGSF
LPPPAPPAASGLAIYLAGGQGQVVGGSVVGPLVASGPVVIMAASFGNAAYERLPLEEEET
PVAVAGNGGLGSPGIPGTQQQPQQQQQQQLVGDPNSSSLFHGMPQNLLNSVQLPAEGYWG
GSARPPF*

Identity of G3456 second conserved domain to G3457 second conserved domain determined using manual alignment = 72/96 identical residues (75.0%)

```
G3456:     VAQFARRRQRGVSILSGSGTVVNVNLRQPTAPGAVMALHGRFDILSLTGSFLPGPSPPGA
           +  FARRRQRGV +LSGSGTV NV LRQP +PGAV+ LHGRF+ILSL+GSFLP P+PP A
G3457:     ITAFARRRQRGVCVLSGSGTVTNVTLRQPASPGAVVTLHGRFEILSLSGSFLPPPAPPAA

G3456:     TGLTIYLAGGQGQIVGGEVVGPLVAAGPVLVMAATF
           +GL IYLAGGQGQ+VGG VVGPLVA+GPV++MAA+F
G3457:     SGLAIYLAGGQGQVVGGSVVGPLVASGPVVIMAASF
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Exhibit C. Polynucleotide subsequences used for hybridization analysis

The best identity match of 50-base subsequences from G3456 and homolog DNAs are listed below and were used for determining theoretical melting temperatures. The first sequence in each pair is the 50 base subsequence derived from G3456 , and the second sequence of each pair is the reverse complement of the corresponding subsequence from each optimally-aligned G3456 homolog. The T_m(conc) (the point at which the concentration of double-stranded molecules of one-half of its maximum value defines the melting temperature) was used to determine theoretical melting temperatures at 0.2x SSC (about 30 mM Na^+) and 2.0x SSC (about 300 mM Na^+). Determinations made with DINAMelt server available at: www.bioinfo.rpi.edu/applications/hybrid/hybrid2.php.

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G3456   CCCTGGGCCGTCCCCTCCCGGCGCCACCGGGCTCACAATCTACCTCGCCG
G3456   CGGCGAGGTAGATTGTGAGCCCGGTGGCGCCGGGAGGGGACGGCCCAGGG
Tm(conc)0.2x SSC: 82.3° C
Tm(conc)2x SSC:   93.6° C


G3456   GCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCAGATCGTCGG
G3460   CCGACGACCTGGCCCTGCCCGCCGGCGAGGTAGATTGTGAGACTGGTGGC
Tm(conc)0.2x SSC: 72.0° C
Tm(conc)2x SSC:   83.3° C


G3456   GCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCAGATCGTCGG
G3459   CCGACAACCTGCCCCTGCCCGCCGGCCAGGTAGATTGTGAGGCTGGTGGC
Tm(conc)0.2x SSC: 71.8° C
Tm(conc)2x SSC:   80.9° C


G3456   GTCACCCGAGACAGCCCTAACGCGCTGCGGAGCCACGTCATGGAGATTGC
G2153   GCGATCTCCATGACATGGCTCTTGAGAGCATTTGGAGAATCGCGAGTGAC
Tm(conc)0.2x SSC: 70.0° C
Tm(conc)2x SSC:   77.3° C


G3456   CCTCCCGGCGCCACCGGGCTCACAATCTACCTCGCCGGAGGCCAGGGGCA
G3401   TGCCCCTGCCCGCCGGCGAGGTACACGGTCAGCCCGGTGGAGCCCGGCGG
Tm(conc)0.2x SSC: 77.2° C
Tm(conc)2x SSC:   86.0° C


G3456   GTGGTGGGCCCACTCGTGGCGGCGGGCCCCGTATTGGTAATGGCGGCTAC
G1073   GAAGCAGCCATCAACACTACCGGTCCCGAAGCAATTAACGAACCAGCCAC
Tm(conc)0.2x SSC: 70.3° C
Tm(conc)2x SSC:   78.7° C
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